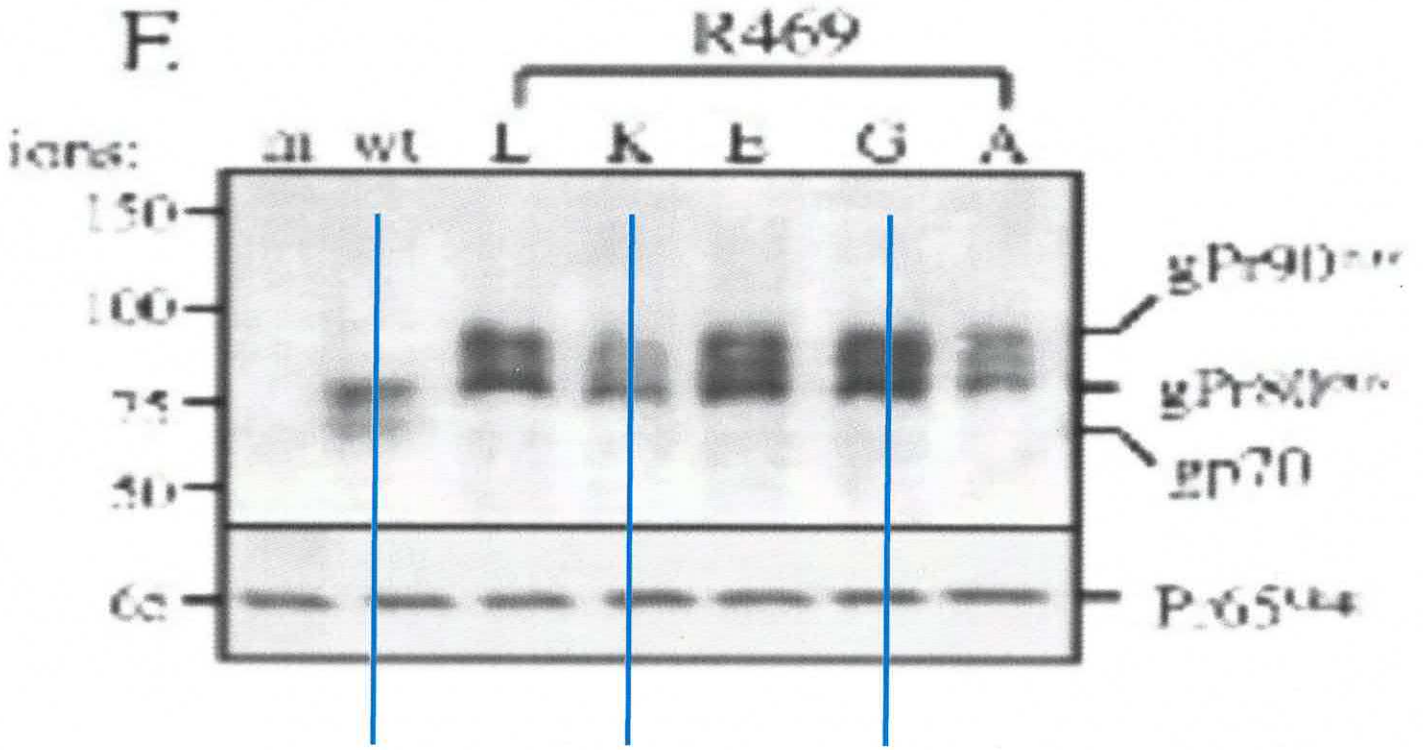
Additional information regarding possible data manipulation/falsification by DA Sanders

Virology; 2010, 405, 214-224; Apte S and Sanders DA
Effect of retroviral envelope protein cleavage upon trafficking, incorporation, and membrane fusion

Figure 1 E. Lines show that the bands do not line up



Additional information #1: Compare Figure 1E to Figures 1B,C, D, F in the same figure. All the lower bands in the other panels are not straight and do match up with the bands above them, indicating that the lower bands in Figure 1E were not from the same experiment (next image)

subunits, SU and TM, at a sequence highly rich in basic amino-acid residues. The minimum enzyme-recognition sequence for most proprotein convertases is Arg-X-Lys/Arg-Arg↓Y (P_4-P_3-P_2-P_1↓P_1' respectively, where ↓ represents cleavage, X represents any residue and Y represents any nonhydrophobic residue) (Henrich et al., 2003, 2005; Rockwell and Fuller, 1998; Rockwell and Fuller, 2002; Rockwell et al., 2002; Rockwell and Thorner, 2004; Schechter and Berger, 1968). After cleavage, the two subunits remain attached covalently resulting in the formation of trimers of SU–TM complexes (Opstelten et al., 1998; Pinter and Fleissner, 1977; Pinter et al., 1997; Sanders, 2000). The virus acquires these Env complexes along with the lipid bilayer while budding through cellular membranes. In the budded virus the viral protease cleaves the last 16 amino acids (the R-Peptide) from the C-terminus of Env thereby disrupting a domain that inhibits fusion by Env in the virus-producing cells (Aguilar et al., 2003; Januszeski et al., 1997; Ragheb and Anderson, 1994; Rein et al., 1994; Taylor and Sanders, 2003).

We have investigated the role of proteolytic processing in the function of the envelope protein in Mo-MuLV. The proprotein-convertases recognition site is highly conserved among retroviruses. By engineering a series of substitution mutations in the enzyme recognition sequence we have obtained evidence that cleavage is indeed essential for virus-induced membrane fusion and envelope glycoprotein incorporation into virions. Additionally, our findings suggest that cleavage plays an important role in the intracellular trafficking of the glycoprotein.

crooked, match up

Straight, do not match up

crooked, match up

crooked, match up

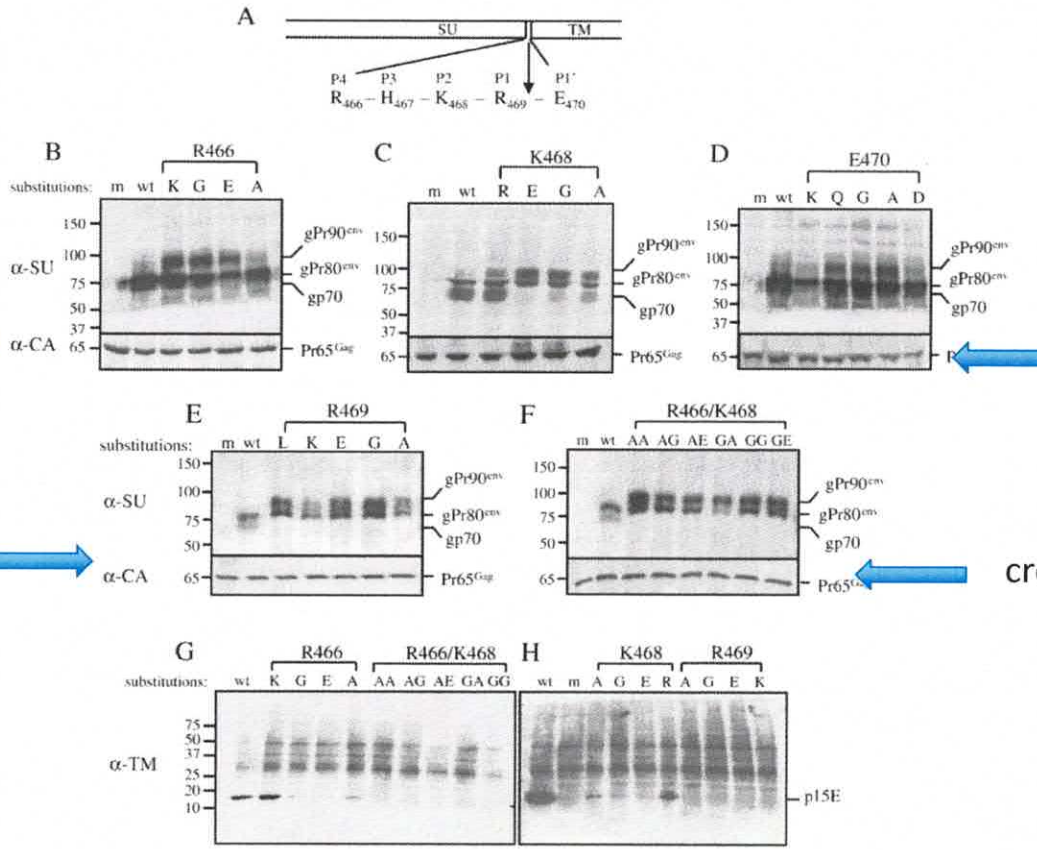
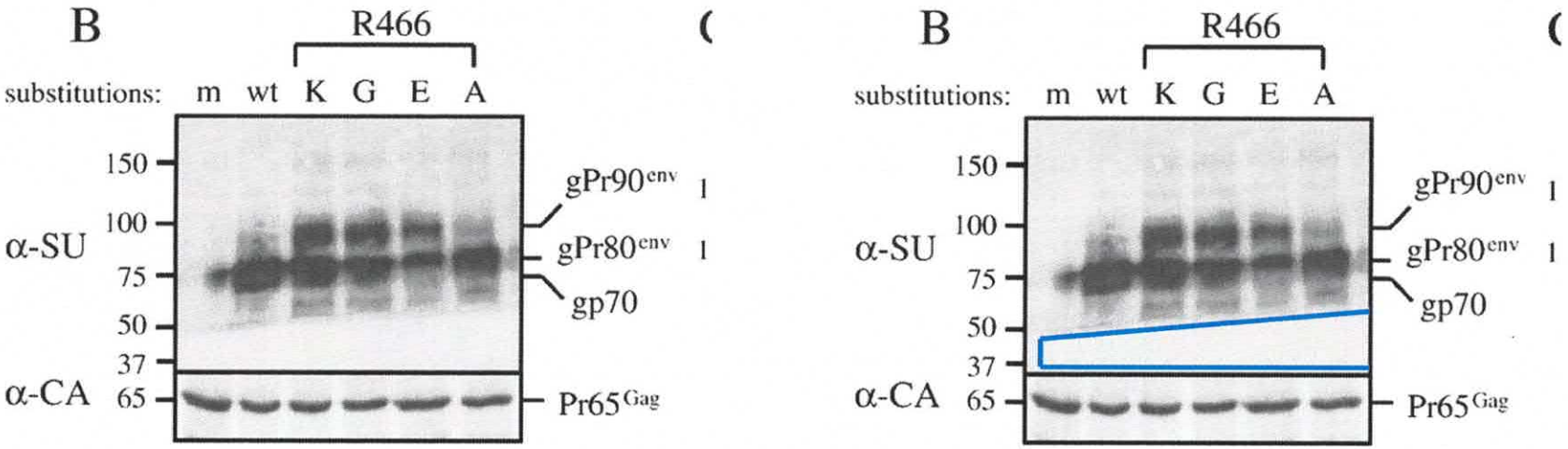
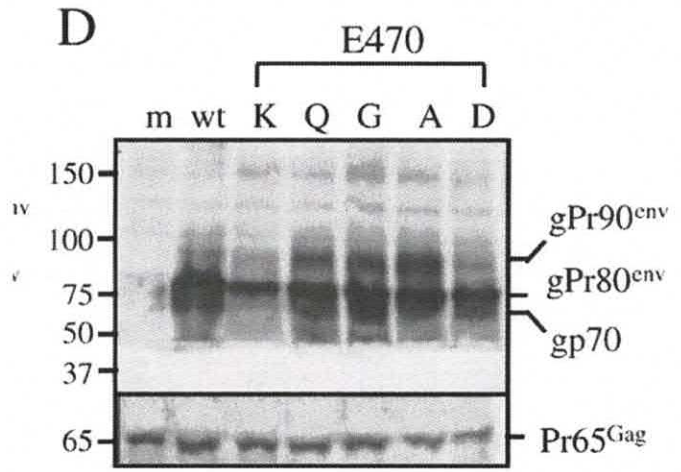


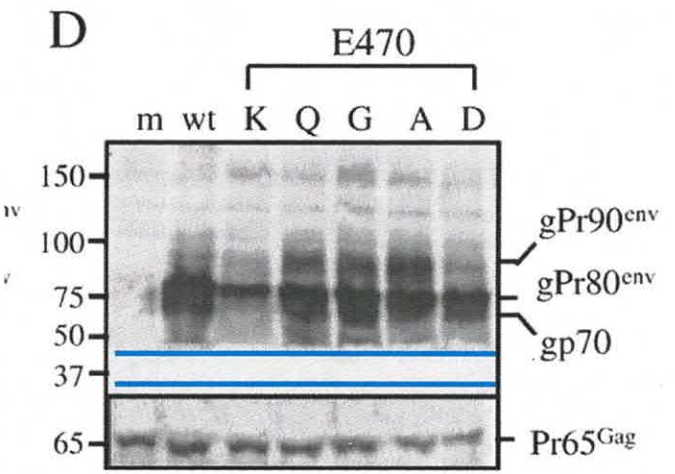
Fig. 1. Mo-MuLV envelope protein cleavage-motif. ↓ represents cleavage site. (A) The positions of the amino-acid residues in the cleavage motif are represented above them and the amino-acid number in the sequence of Moloney murine leukemia virus envelope protein is represented in subscript. (B–F) Analysis of the proteolytic processing of Mo-MuLV envelope proteins: The cell lysates from Φ-NXnlslacZ cells expressing wild-type or mutant envelope proteins were analyzed by SDS-PAGE (9% acrylamide). The proteins were transferred to the nitrocellulose membranes and probed with α-SU (anti-Rauscher gp70 antibody) (B–F upper panels) and α-CA (anti-p30 antibody) antibodies (B–F lower panels) separately. Three species of Env are detected by anti-SU antibody: $gPr90^{env}$ (90 kDa) fully *N*- and O-glycosylated and uncleaved Env, $gPr80^{env}$ (80 kDa), an endo-H sensitive, high mannose glycosylated Env, and gp70 (SU) (70 kDa); their positions of migration are indicated on the right. Molecular size marker is represented on the left with the sizes in kDa. Anti-capsid antibody recognizes $Pr65^{Gag}$ protein (65 kDa). (G and H) Immunoblot analysis using α-TM antibody was performed. The cell lysates were analyzed using 10–20% acrylamide gradient gels. A 15 kDa p15E (TM) band is detected by the monoclonal anti-TM antibody. 'wt' represents wild-type envelope protein and 'm' (mock) represents cells transfected with empty vector. In the α-SU panel of B, a small volume of protein from the wt lane has leaked into the mock lane.

Additional information #2: Look at Figure 1B in the same figure. Notice that there is a wedge of the gel where the background, clearly evident above and below, has been lost suggesting that this part of the image was intentionally removed to hide some data (blue lines in right image)



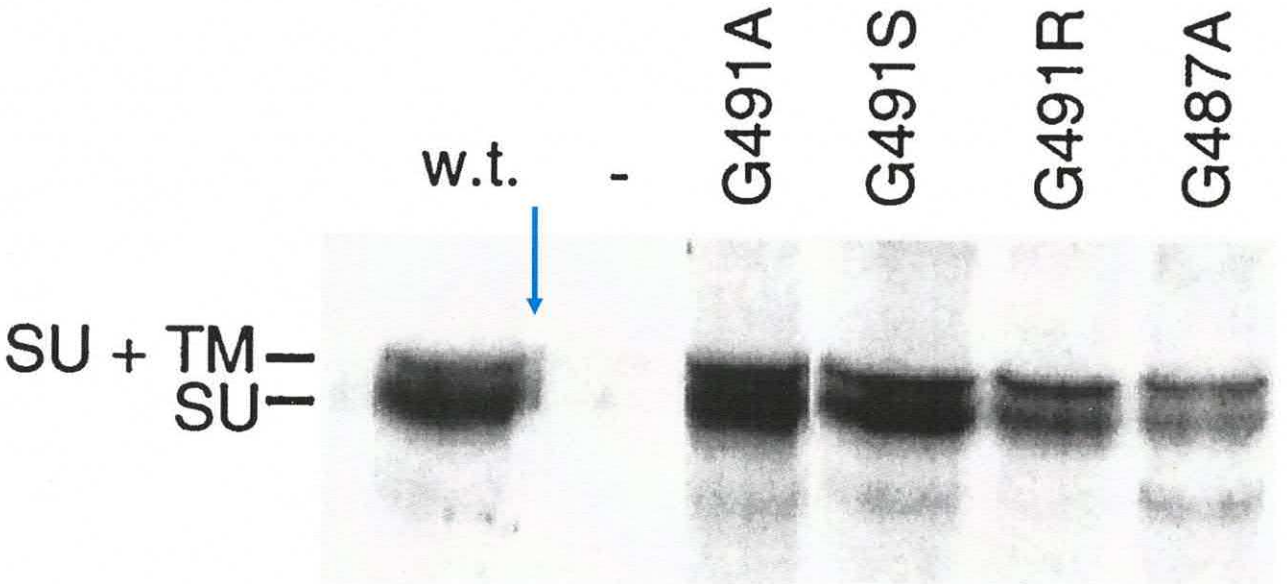
Additional information #3: Look at Figure 1D in the same figure. Notice that there is a wedge of the gel where the background, clearly evident above and below, has been lost suggesting that this part of the image was intentionally removed to hide some data (blue lines in right image). Compare this to the other panels in this figure where these abrupt loss of background are not evident





Taylor GM, Gao Y, Sanders DA. Fv-4: identification of the defect in Env and the mechanism of resistance to ecotropic murine leukemia virus. J Virol. 2001 Nov;75(22):11244-8.

Additional information #4: Look at Figure 3. The w.t band appears to be superimposed on another band (arrow) and the – control shows none of the background seen in the other bands



Taylor GM, Sanders DA. The role of the membrane-spanning domain sequence in glycoprotein-mediated membrane fusion. Mol Biol Cell. 1999 Sep;10(9):2803-15

Additional information #5: Look at Figure 3. The G and V bands appear to be the same with the V band raised a bit and is darker. Note that each has the same white clear area in the centre (arrows). This white clear column is better seen in the original paper. Also note that the Proline-617 image is the only one where the 3 lanes are far apart